Figure S1. Distribution of cells in the G1, S-phase and G2 at different time points after ionizing irradiation of HEKn cell lines with 2 and 6 Gy. All indicated values in the figure apply only to cells in the G2 phase. ns, not significant. No significant differences were noted for the proportion of cells in G1 and S after treatment as also indicated in the text of the results section. HEKn, human epithelial keratinocytes.

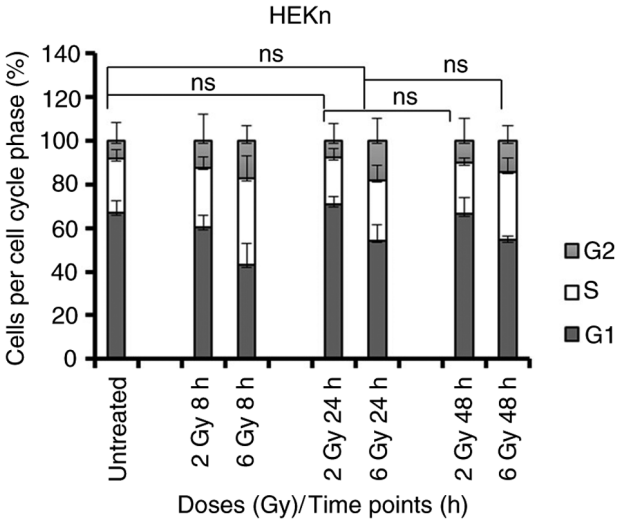

Figure S2. Flow cytometry plot of the distribution of cells in G1, S-phase and G2 at different time points after ionizing irradiation (2 and 6 Gy) for HPV$^+$ and HPV$^-$ cell lines. HPV$^+$ cell lines with 2 Gy (A-E) with 6 Gy (F-J) and HPV$^-$ cell lines with 2 Gy (K-O) with 6 Gy (P-T) after 8, 24 and 48 h. This shows one represenative flow cytometry plot (FL2-A::FL2-A). HPV, human papillomavirus.

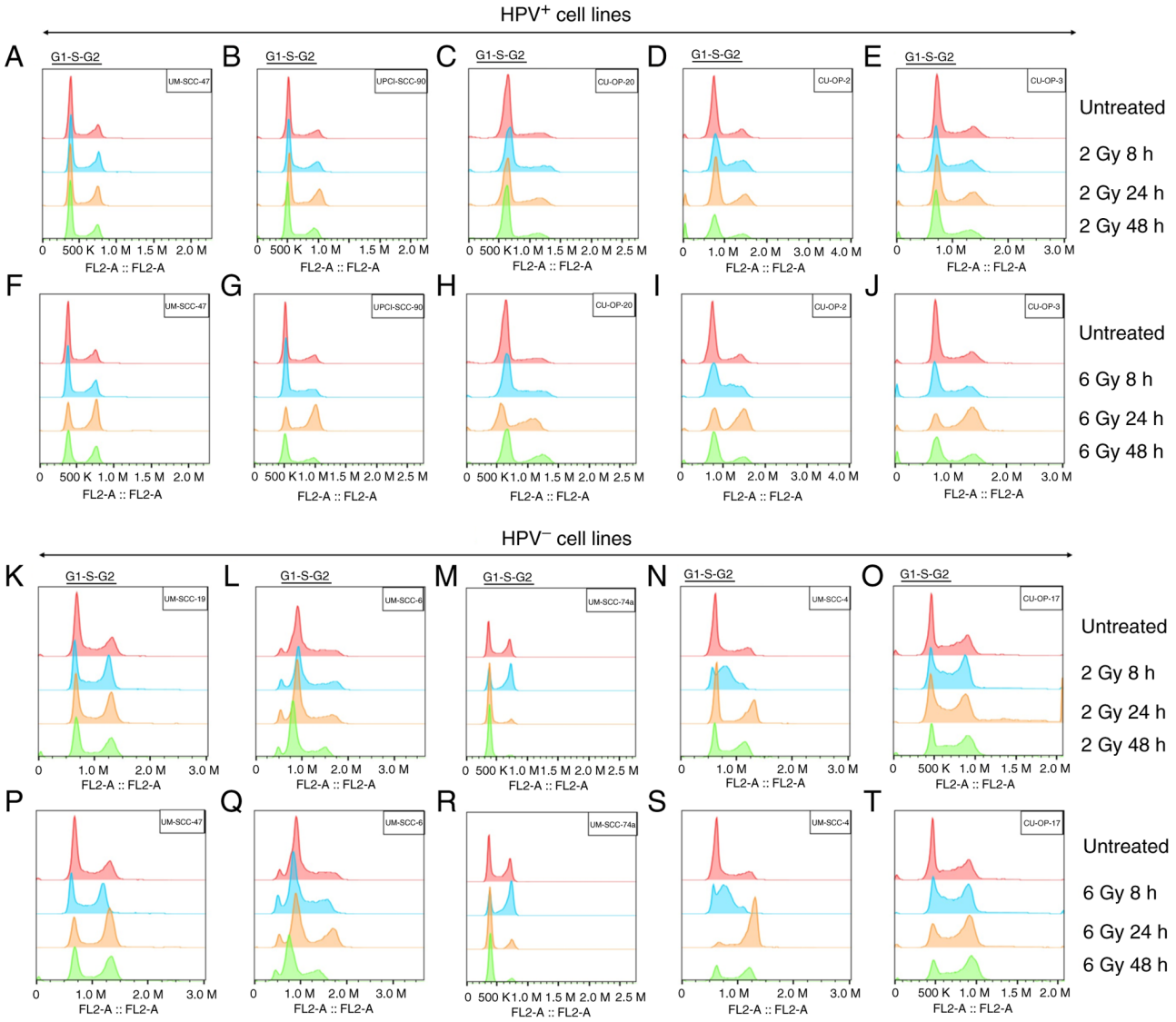

Figure S3. Flow cytometry plot of the distribution of cells of in G1, S-phase and G2 at different time points after ionizing irradiation of HEKn cell lines with 2 and 6 Gy. HPV$^{+}$ cell lines with (A) 2 Gy and (B) 6 Gy after 8, 24 and 48 h. This shows one represenative flow cytometry plot (FL2-A::FL2-A). HEKn, human epithelial keratinocytes.

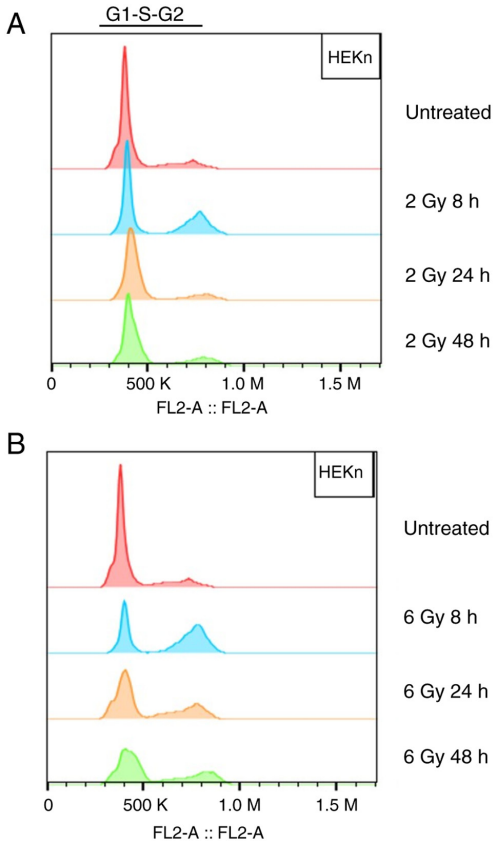

Figure S4. Circos plots visualizing HPV integration of radiosensitive and radioresistant HPV$^+$ cell lines before and after ionizing irradiation. Human chromosomes and HPV-16 sequence are not to scale. (A) Radiosensitive cell lines and (B) radioresistant cell lines. Fusion transcripts are indicated as grey lines for mapped reads between the HPV-16 sequence and the human genome at various chromosome sites. Increased numbers of chromosome sites has to be seen as basic interpretation of rise in numbers. Strengths of the lines indicate number of reads detected. Details of exact numbers are presented in the text of the results section. HPV, human papillomavirus.

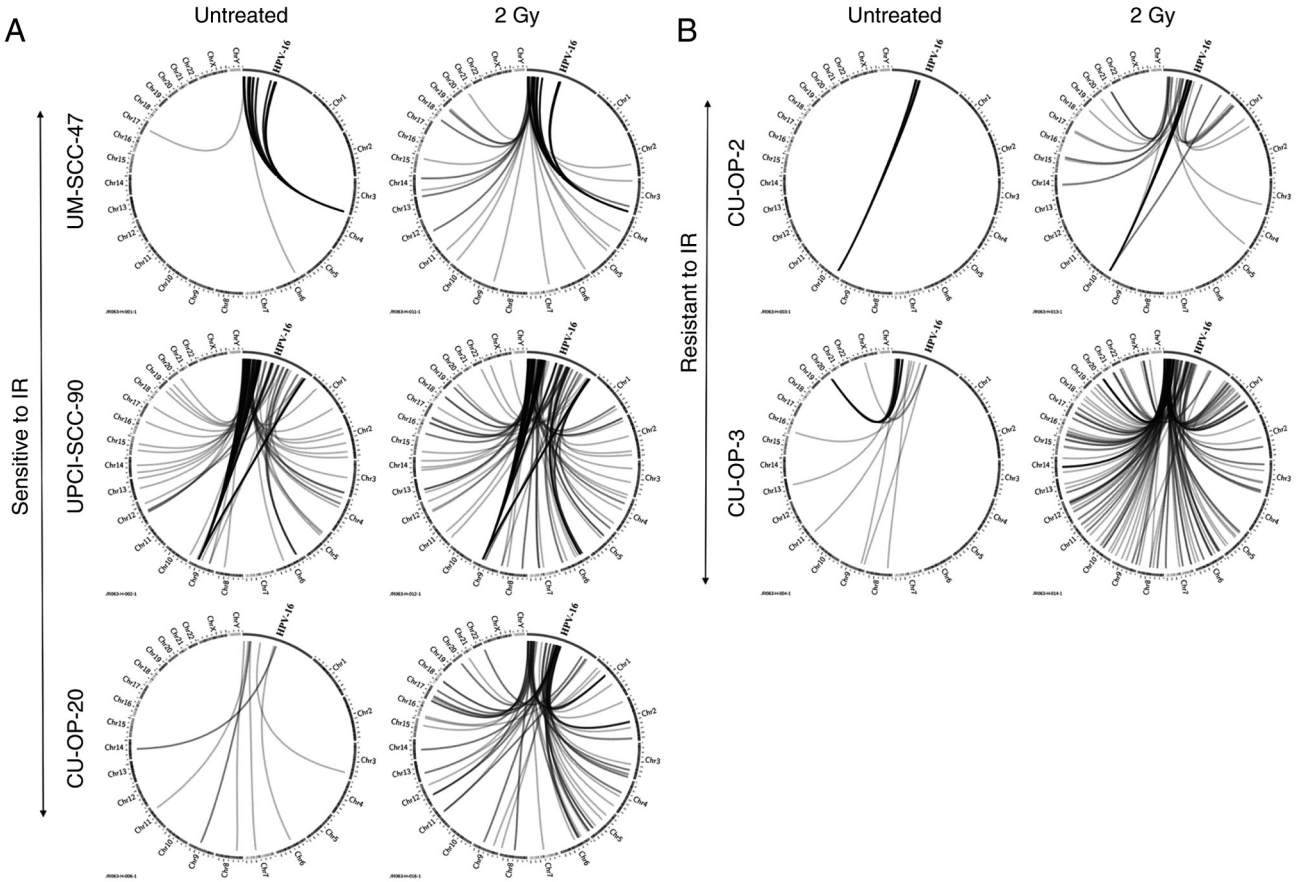

Table SI. Of the 519 transcripts with significant changes after 24 h treatment of HPV$^+$ and HPV$^-$ cell lines with 2 Gy, the top 19 genes are presented.

| Genes[a] | Description | ID | FDR P-value | log2FC[b] |
|---|---|---|---|---|
| *EEF1E1* | Eukaryotic translation elongation factor 1 epsilon 1 | NM_004280_chr6 | 1.1E-05 | 0.66 |
| *ITPRIP* | Inositol 1,4,5-trisphosphate receptor interacting protein | NM_033397_chr10 | 1.7E-05 | -0.59 |
| *NDUFAF4* | NADH: Ubiquinone oxidoreductase complex assembly factor 4 | NM_014165_chr6 | 1.7E-05 | 0.69 |
| *SH3TC1* | SH3 domain and tetratricopeptide repeats 1 | NM_018986_chr4 | 5.0E-05 | -0.72 |
| *GNB4* | G protein subunit β 4 | NM_021629_chr3 | 6.4E-05 | 0.58 |
| *PNPT1* | Polyribonucleotide nucleotidyltransferase 1 | NM_033109_chr2 | 7.1E-05 | 0.59 |
| *POLR3G* | RNA polymerase III subunit G | NM_006467_chr5 | 1.7E-05 | 0.83 |
| *MTR* | 5-methyltetrahydrofolate-homocysteine methyltransferase | NM_000254_chr1 | 3.6E-04 | 0.38 |
| *MIR3687-1* | MicroRNA 3687-1 | NR_037458_chr21 | 3.6E-04 | -0.98 |
| *RPL22L1* | Ribosomal protein L22 like 1 | NM_001099645_chr3 | 3.6E-04 | 0.68 |
| *GNPNAT1* | Glucosamine-phosphate N-acetyltransferase 1 | NM_198066_chr14 | 4.0E-04 | 0.51 |
| *AGPAT5* | 1-acylglycerol-3-phosphate O-acyltransferase 5 | NM_018361_chr8 | 4.0E-04 | 0.53 |
| *CASD1* | CAS1 domain containing 1 | NM_022900_chr7 | 8.4E-04 | 0.52 |
| *RPF2* | Ribosome production factor 2 homolog | NM_032194_chr6 | 9.1E-04 | 0.50 |
| *EPHB3* | EPH receptor B3 | NM_004443_chr3 | 9.1E-04 | -0.62 |
| *TWISTNB* | TWIST neighbour | NM_001002926_chr7 | 9.5E-04 | 0.51 |
| *P3H2* | Prolyl 3-hydroxylase 2 | NM_018192_chr3 | 9.5E-04 | -0.73 |
| *GSN* | Gelsolin | NM_000177_chr9 | 1.4E-03 | -0.95 |
| *OTUD6B* | OTU domain containing 6B | NM_016023_chr8 | 2.4E-03 | 0.57 |

[a]The 19 most significant genes are presented. [b]log2FC, fold change of the significant presented gene. HPV, human papillomavirus; FDR, false discovery rate.